WHAT IS CLAIMED IS:

1.   An antigen presenting cell (APC) expressing at least two fusion proteins, wherein (i) each of the fusion proteins comprise an MHC molecule portion and a reporter peptide portion, and (ii) the reporter peptide portion of each fusion protein is detectably different from the reporter peptide portion of every other of the at least two fusion proteins and the MHC molecule portion of each fusion protein is different from the MHC molecule portion of every other of the at least two fusion proteins.

2.   The APC of claim 1, wherein the reporter peptide portions of the at least two fusion proteins are fluorescent and fluoresce at detectably different wavelengths from one another.

3.   The APC of claim 1 or claim 2, wherein the APC is prepared from a human cell.

4.   A human APC that expresses a fusion protein comprising a human leukocyte antigen HLA-A*201 portion and a reporter peptide portion.

5.   The APC of claim 4, wherein the reporter peptide portion comprises the amino acid sequence of a green fluorescent protein.

6.   A method for determining whether a T cell specific for a peptide is present in a population of cells, which method comprises:

(a)   introducing the peptide into an APC, which expresses a fusion protein comprising (i) a major histocompatibility complex (MHC) molecule portion and (ii) a reporter peptide portion, the peptide such that a complex forms between the fusion protein and the peptide and the peptide is displayed by the APC,

(b)   contacting the APC displaying the complex with a population of cells, such that T cells in the population of cells specific for the antigen will detectably internalize the complex,

32

(c)   determining T cells in the population of cells have detectably internalized the complex,

whereupon T cells which are in the population of cells and are specific for the peptide are determined to be present.

7.   The method of claim 6, wherein the population of cells are human cells.

8.   The method of claim 6 or 7, wherein the population of cells consists essentially of human peripheral blood mononuclear cells (PBMCs).

9.   The method of any one of claims 6-8, wherein the method comprises repeating steps (a)-(c) until T cells in the population have internalize the complex, whereupon a T cell specific for the antigen is identified, wherein a different population of cells contacts the APC displaying the complex in each repetition of steps (a)-(c).

10.   A method for quantifying the number of T cells, which are specific for an epitope of interest, in a population of cells comprising T cells, which method comprises:

(a)   introducing a peptide comprising the epitope of interest into an APC, which expresses a fusion protein comprising (i) an MHC molecule portion which binds an epitope of interest and (ii) a reporter peptide portion, a peptide comprising the epitope of interest such that a complex forms between the fusion protein and the peptide and the peptide is displayed by the APC,

(b)   contacting the APC displaying the peptide with a population of cells comprising T cells, such that those T cells in the population of cells specific for the epitope detectably internalize the complex, and

(c)   determining how many T cells in the population of cells have internalized the complex, whereupon T cells, which are in the population of cells and are specific for the epitope of interest, are quantified.

11.   The method of claim 10, wherein the population of cells consists essentially of human PBMCs.

12.   The method of claim 10 or claim 11, wherein the reporter peptide portion comprises the amino acid sequence of a fluorescent polypeptide.

13.   The method of any one of claims 10-12, wherein the method comprises comparing the number of T cells determined in step (d) with an enumeration of the antigen-specific T cells in the population obtained through tetramer analysis or cytokine secretion analysis.

14.   The method of any one of claims 10-13, wherein the T cells are primate T cells.

15.   The method of claim 14, wherein the T cells are human T cells.

16.   The method of any one of claims 12-15 wherein the peptide is introduced into the APC by (a) expressing a nucleic acid in the APC that encodes a polypeptide that comprises the peptide or (b) contacting the APC with a polypeptide that comprises the peptide, wherein the APC processes the polypeptide to produce the peptide.

17.   A method for determining whether a peptide induces a T cell-mediated immune response comprising:
        (a)   introducing the peptide into an APC, which expresses a fusion protein comprising (i) an MHC molecule portion and (ii) a reporter peptide portion, the peptide under conditions where a complex can form between the fusion protein and the peptide and the peptide is displayed by the APC,
        (b)   contacting the APC displaying the peptide with a population of T cells, such that T cells in the population specific for the peptide detectably internalize the complex, and
        (c)   detecting whether cells in the population of T cells have internalized the complex,
        whereupon the peptide is determined to induce a T cell-mediated immune response.

18.   The method of claim 17, wherein the peptide is a portion of a polypeptide.

19.   The method of claim 18, wherein the polypeptide is known to induce a T cell response.

20.   The method of claim 17, wherein the peptide is introduced into the APC by (a) expressing a nucleic acid in the APC that encodes a polypeptide that consists essentially of the peptide or (b) contacting the APC with a polypeptide that consists essentially of the peptide, wherein the APC processes the polypeptide to produce the peptide.

21.   The method of claim 20, wherein the nucleic acid comprises part of a viral genome.

22.   The method of claim 21, wherein the viral genome is a recombinant viral genome and the polypeptide is a nonviral polypeptide or a viral polypeptide not expressed by the viral genome associated with the virus from which the genome was obtained or derived.

23.   The method of any one of claims 18-22, wherein the polypeptide is selected from a number of polypeptides collectively known to induce a T cell response.

24.   The method of claim 17, wherein the peptide introduced into the APC is about 7-25 amino acids in length.

25.   The method of any one of claims 17-24, wherein the method comprises repeating steps (a)-(c) each time with a different peptide, until T cells in the population of T cells have internalized the complex.

26.   The method of claim 25, wherein a portion of the amino acid sequence of each peptide is identical to a portion of the amino acid sequence of at least one other peptide.

27.   The method of any one of claims 17-26, wherein the peptide is associated with an autoimmune disease in a human, a cancer or a virus.

28.   The method of any one of claims 17-27, wherein the peptide is an altered peptide ligand (APL) derived from an antigenic peptide by the addition, substitution, or deletion of one or more amino acid residues in the antigenic peptide.

29.   A method of monitoring the efficacy of treatment of a disease in a patient, which method comprises comparing the number of T cells, which are specific for one or more epitopes of interest, which can be from one or more antigens of interest, in a population of cells comprising T cells obtained from the patient before treatment and in a population of cells comprising T cells obtained from the patient during and/or after treatment,

wherein the number of T cells are determined in accordance with the method of claim 1,

wherein, when the treatment induces a T cell-mediated response, an increase in the number of T cells after treatment as compared to the number of T cells before treatment indicates that the treatment is efficacious, whereas no change in the number of T cells or a decrease in the number of T cells after treatment as compared to the number of T cells before treatment indicates that the treatment is not efficacious, and

wherein, when the treatment inhibits a T cell-mediated response, no change in the number of T cells or a decrease in the number of T cells after treatment as compared to the number of T cells before treatment indicates that the treatment is efficacious, whereas an increase in the number of T cells after treatment as compared to the number of T cells before treatment indicates that the treatment is not efficacious.

30.   The method of claim 29, wherein the disease is mediated by a pathological T cell response.

31.   The method of claim 29, wherein:

(a)   the disease is an autoimmune disease and the one or more epitopes of interest is/are autoimmune epitope(s);

(b)   the disease is diabetes and the one or more epitopes of interest is/are epitopes from an islet of Langerhans cell;

(c)   the disease is arthritis and the one or more epitopes of interest is/are from collagen;

(d)   the disease is multiple sclerosis and the one or more epitopes of interest is/are from myelin or an antigen of the central nervous system;

(e)   the disease results from infection with a virus and the one or more epitopes of interest is/are from the virus; or

(f)   the virus is human immunodeficiency virus (HIV), a species of Vaccinia, hepatitis virus, or cytomegalovirus (CMV).

32.   The method of claim 31, wherein the disease results from infection with a bacterium and the one or more epitopes of interest is/are from the bacterium.

33.   The method of claim 32, wherein the bacterium is a species of Chlamydia, Helicobacter or Mycobacteria.

34.   The method of claim 29, wherein the disease results from infection with a parasite and the one or more epitopes of interest is/are from the parasite.

35.   The method of claim 29, wherein the treatment comprises vaccination or immunization against the disease.

36.   The method of claim 29, wherein the disease is anthrax, measles, rubella or cancer.

37.   A method of evaluating the immunological effect of an antigen on the phenotypic or functional activity profile of a population of T cells comprising:

(a)   introducing the antigen into an APC, which expresses a fusion protein comprising (i) an MHC molecule portion and (ii) a reporter peptide portion, the antigen such that a complex forms between the fusion protein and the antigen and the antigen is displayed by the APC,

(b)   contacting the APC displaying the antigen with a population of T cells comprising T cells specific for the antigen and characterized by a phenotypic trait or functional trait, such that at least some of the T cells detectably internalize the complex, and

(c)   characterizing the population of T cells on the basis of (i) the phenotypic trait, (ii) the functional trait, (iii) a second phenotypic trait that differs from the phenotypic

trait, (iv) a second functional trait that differs from the functional trait, or (v) any combination of (i)-(iv),

whereupon the immunological effect of the antigen on the phenotypic or functional activity profile of the population of T cells is evaluated.

38.   The method of claim 37, wherein the method comprises characterizing the population of T cells on the basis of the number of T cells in the population that comprise one or more cell surface markers.

39.   The method of claim 38, wherein the one or more cell surface markers are selected from the group consisting of CD27, CD28, CCR7, CD45RA, CD45RO, and combinations thereof.

40.   The method of any one of claims 37-39, wherein the method comprises characterizing the population of T cells on the basis of perforin expression level.

41.   The method of any one of claims 37-40, wherein the T cells are cytolytic lymphocytes (CTLs) and the method comprises characterizing the population of T cells on the basis of the cytolytic activity of the T cells with respect to one or more target cells.

42.   The method of claim 37, wherein the T cells are CD4+ T cells and the method comprises characterizing the T cells on the basis of cytokine and/or chemokine secretion from or expression in the T cells.

43.   The method of claim 37, wherein the phenotypic trait or functional trait detectably changes in association with the maturity of the T cells, whereupon the method provides a method for assessing the maturity level of the T cells.

44.   The method of claim 37, wherein the antigen is associated with disease-causing cells and the method further comprises repeating step (c) over time and characterizing the population of T cells on the basis of (i) the phenotypic trait or (ii) the

38

functional trait, whereupon the effectiveness of a T-cell-mediated response to the antigen is
assessed.

45.   The method of claim 37, wherein the phenotypic trait or functional trait
detectably changes as T cells mature and the method further comprises repeating step (c)
over time and characterizing the population of T cells on the basis of (i) the phenotypic trait
or (ii) the functional trait, whereupon the maturity of the T cells is assessed.

46.   A method of preparing a targeted pharmaceutical composition for
ameliorating a disease associated with T cell activity in a mammal comprising performing
the method of claim 20, characterizing the peptide that induces a T cell-mediated immune
response and associating (i) an antigenic peptide comprising an amino acid sequence
consisting essentially of the amino acid sequence of the amino acid sequence of the peptide
and (ii) a molecule that inhibits the proliferation and/or activity of T cells, whereupon a
targeted pharmaceutical composition for ameliorating a disease associated with T cell
activity in a mammal is prepared.

47.   The method of claim 46, wherein the antigenic peptide comprises the amino
acid sequence of the peptide internalized by the cells.

48.   The method of claim 46 or claim 47, wherein the antigenic peptide is
conjugated to a toxin.

49.   The method of claim 46, wherein the antigenic peptide comprises a first
peptide portion comprising the amino acid sequence of the peptide internalized by the T
cells fused to a second peptide portion comprising an amino acid sequence that promotes
apoptosis of T cells.

50.   The method of any one of claims 46-49, wherein the disease is an
autoimmune disease that afflicts humans.